

David

1646

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/214,982

DATE: 11/09/1999
TIME: 11:28:34

Input Set: I214982.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

P.S.

ENTERED

1 <110> APPLICANT: Hirata, Yuichi
2 Nezu, Junichi
3 <120> TITLE OF INVENTION: Novel VEGF-like Factor
4 <130> FILE REFERENCE: 50026/014001
5 <140> CURRENT APPLICATION NUMBER: US/09/214,982
6 <141> CURRENT FILING DATE: 1999-01-14
7 <150> EARLIER APPLICATION NUMBER: 8-185216 Japan
8 <151> EARLIER FILING DATE: 1996-07-15
9 <160> NUMBER OF SEQ ID NOS: 34
10 <170> SOFTWARE: FastSEQ for Windows Version 4.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 354
13 <212> TYPE: PRT
14 <213> ORGANISM: Homo sapiens
15 <400> SEQUENCE: 1
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17 1 5 10 15
18 Gln Leu Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser
19 20 25 30
20 Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
21 35 40 45
22 Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
23 50 55 60
24 Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
25 65 70 75 80
26 Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
27 85 90 95
28 Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
29 100 105 110
30 Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
31 115 120 125
32 Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
33 130 135 140
34 Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
35 145 150 155 160
36 Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
37 165 170 175
38 Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
39 180 185 190
40 Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
41 195 200 205
42 Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
43 210 215 220
44 Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu

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45      225      230      235      240
46      Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
47              245      250      255
48      Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
49              260      265      270
50      Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
51              275      280      285
52      Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
53              290      295      300
54      Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
55      305      310      315      320
56      His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys
57              325      330      335
58      Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
59              340      345      350
60      Asn Pro
61      <210> SEQ ID NO 2
62      <211> LENGTH: 2004
63      <212> TYPE: DNA
64      <213> ORGANISM: Homo sapiens
65      <220> FEATURE:
66      <221> NAME/KEY: CDS
67      <222> LOCATION: (403)...(1464)
68      <400> SEQUENCE: 2
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70      cctgcggcat acattggaga gattttttta attttctgga caygaagtaa atttagagtg      120
71      ctttcyaatt tcaggtagaa gacatgtcca ctttctgatt atttttggag aacattttga      180
72      tttttttcat ctctctctcc ccaccctaa gattgtgcaa aaaaagcgta ccttgccata      240
73      ttgaaataat ttcatggat tttgatcaga actgatcatt tggttttctg tgtgaagttt      300
74      tgaggtttca aactttcctt ctggagaatg ctttttgaaa caattttctc tagctgctg      360
75      atgtcaactg cttagtaatc agtggatatt gaaatattca aa atg tac aga gag      414
76                                  Met Tyr Arg Glu
77                                  1
78      tgg gta gtg gtg aat gtt ttc atg atg ttg tac gtc cag ctg gtg cag      462
79      Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu Val Gln
80      5      10      15      20
81      ggc tcc agt aat gaa cat gga cca gtg aag cga tca tct cag tcc aca      510
82      Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser Ser Gln Ser Thr
83              25      30      35
84      ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg gag gaa      558
85      Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu Glu Glu
86              40      45      50
87      cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga tgc agg      606
88      Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg Cys Arg
89              55      60      65
90      ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca tcc cat      654
91      Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg Ser Ala Ser His
92              70      75      80
93      cgg tcc act agg ttt gcg gca act ttc tat gac att gaa aca cta aaa      702
94      Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile Glu Thr Leu Lys

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95	85	90	95	100	
96	ggt ata gat gaa gaa tgg caa aga act cag tgc agc cct aga gaa acg				750
97	Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg Glu Thr				
98		105	110	115	
99	tgc gtg gag gtg gcc agt gag ctg ggg aag agt acc aac aca ttc ttc				798
100	Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr Asn Thr Phe Phe				
101		120	125	130	
102	aag ccc cct tgt gtg aac gtg ttc cga tgt ggt ggc tgt tgc aat gaa				846
103	Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly Cys Cys Asn Glu				
104		135	140	145	
105	gag agc ctt atc tgt atg aac acc agc acc tcg tac att tcc aaa cag				894
106	Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr Ile Ser Lys Gln				
107		150	155	160	
108	ctc ttt gag ata tca gtg cct ttg aca tca gta cct gaa tta gtg cct				942
109	Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro Glu Leu Val Pro				
110		165	170	175	180
111	ggt aaa gtt gcc aat cat aca ggt tgt aag tgc ttg cca aca gcc ccc				990
112	Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu Pro Thr Ala Pro				
113		185	190	195	
114	cgc cat cca tac tca att atc aga aga tcc atc cag atc cct gaa gaa				1038
115	Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln Ile Pro Glu Glu				
116		200	205	210	
117	gat cgc tgt tcc cat tcc aag aaa ctc tgt cct att gac atg cta tgg				1086
118	Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile Asp Met Leu Trp				
119		215	220	225	
120	gat agc aac aaa tgt aaa tgt gtt ttg cag gag gaa aat cca ctt gct				1134
121	Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu Asn Pro Leu Ala				
122		230	235	240	
123	gga aca gaa gac cac tct cat ctc cag gaa cca gct ctc tgt ggg cca				1182
124	Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala Leu Cys Gly Pro				
125		245	250	255	260
126	cac atg atg ttt gac gaa gat cgt tgc gag tgt gtc tgt aaa aca cca				1230
127	His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys Thr Pro				
128		265	270	275	
129	tgt ccc aaa gat cta atc cag cac ccc aaa aac tgc agt tgc ttt gag				1278
130	Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys Phe Glu				
131		280	285	290	
132	tgc aaa gaa agt ctg gag acc tgc tgc cag aag cac aag cta ttt cac				1326
133	Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu Phe His				
134		295	300	305	
135	cca gac acc tgc agc tgt gag gac aga tgc ccc ttt cat acc aga cca				1374
136	Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr Arg Pro				
137		310	315	320	
138	tgt gca agt ggc aaa aca gca tgt gca aag cat tgc cgc ttt cca aag				1422
139	Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe Pro Lys				
140		325	330	335	340
141	gag aaa agg gct gcc cag ggg ccc cac agc cga aag aat cct				1464
142	Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro				
143		345	350		
144	tgattcagcg ttccaagttc cccatccctg tcatttttaa cagcatgctg ctttgccaag				1524

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145      ttgctgtcac tgtttttttt ccaggtgtta aaaaaaaaaa ccattttaca cagcaccaca 1584
146      gtgaatccag accaaccttc cattcacacc agctaaggag tccctgggtc attgatggat 1644
147      gtcttctagc tgcagatgcc tctgcgcacc aaggaatgga gaggagggga cccatgtaat 1704
148      ccttttgttt agttttgttt ttgttttttg gtgaatgaga aaggtgtgct ggtcatggaa 1764
149      tggcaggtgt catatgactg attactcaga gcagatgagg aaaactgtag tctctgagtc 1824
150      ctttgcta at cgcaactctt gtgaattatt ctgattcttt tttatgcaga atttgattcg 1884
151      tatgatcagt actgactttc tgattactgt ccagcttata gtcttccagt ttaatgaact 1944
152      accatctgat gtttcatatt taagtgtatt taaagaaaat aaacaccatt attcaagtct 2004
153      <210> SEQ ID NO 3
154      <211> LENGTH: 16
155      <212> TYPE: PRT
156      <213> ORGANISM: Homo sapiens
157      <400> SEQUENCE: 3
158      Cys Gly Pro Asn Lys Glu Leu Asp Glu Asn Thr Cys Gln Cys Val Cys
159      1          5          10          15
160      <210> SEQ ID NO 4
161      <211> LENGTH: 27
162      <212> TYPE: DNA
163      <213> ORGANISM: Artificial Sequence
164      <220> FEATURE:
165      <223> OTHER INFORMATION: Synthetic DNA
166      <400> SEQUENCE: 4
167      agggatgggg aacttggaac gctgaat 27
168      <210> SEQ ID NO 5
169      <211> LENGTH: 27
170      <212> TYPE: DNA
171      <213> ORGANISM: Artificial Sequence
172      <220> FEATURE:
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174      <400> SEQUENCE: 5
175      gatcta atcc agcacc ccaa aaactgc 27
176      <210> SEQ ID NO 6
177      <211> LENGTH: 27
178      <212> TYPE: DNA
179      <213> ORGANISM: Artificial Sequence
180      <220> FEATURE:
181      <223> OTHER INFORMATION: Synthetic DNA
182      <400> SEQUENCE: 6
183      ccatccta at acgact cact atagggc 27
184      <210> SEQ ID NO 7
185      <211> LENGTH: 33
186      <212> TYPE: DNA
187      <213> ORGANISM: Artificial Sequence
188      <220> FEATURE:
189      <223> OTHER INFORMATION: Synthetic DNA
190      <400> SEQUENCE: 7
191      ctggttcggc ccagaacttg gaacgctgaa tca 33
192      <210> SEQ ID NO 8
193      <211> LENGTH: 32
194      <212> TYPE: DNA

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195 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Synthetic DNA
198 <400> SEQUENCE: 8
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201 <211> LENGTH: 20
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Synthetic DNA
206 <400> SEQUENCE: 9
207      aattaaccct cactaaaggg          20
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209 <211> LENGTH: 22
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Synthetic DNA
214 <400> SEQUENCE: 10
215      ccagggtttt cccagtcacg ac          22
216 <210> SEQ ID NO 11
217 <211> LENGTH: 23
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Synthetic DNA
222 <400> SEQUENCE: 11
223      actcactata gggctcgagc ggc          23
224 <210> SEQ ID NO 12
225 <211> LENGTH: 17
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: Synthetic DNA
230 <400> SEQUENCE: 12
231      aagtctggag acctgct          17
232 <210> SEQ ID NO 13
233 <211> LENGTH: 17
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: Synthetic DNA
238 <400> SEQUENCE: 13
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240 <210> SEQ ID NO 14
241 <211> LENGTH: 17
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
      <220> FEATURE:

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION US/09/214,982DATE: 11/09/1999
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Line	Error/Warning	Original Text
404	W "N" or "Xaa" used: Feature required	gtgattcccc agttcactga caaatgactt gtagcttc